

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar

(ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Heller Ehrman White & McAuliffe
(B) STREET: 4350 La Jolla Village Drive, 6th Floor
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92122

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/835,682
(B) FILING DATE: 10-APR-1997
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/695,191
(B) FILING DATE: 07-AUG-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/682,080
(B) FILING DATE: 15-JUL-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1293 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (iii) MOLECULE TYPE: Genomic DNA
- (iv) HYPOTHETICAL: NO
- (v) ANTISENSE: NO
- (vi) FRAGMENT TYPE:
- (vii) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTATCATCA	TTTTTCAGNT	CCTCAAGTGG	AATGTTCTCA	TTTNCCTAAGA	TTTTAAAGTTT	60
TCTCGCCATA	TTCTCTGGTC	TACAGTGTGC	ATTTCCTCAT	TTNCAGCTTG	CAGTTTCTGAT	120
TTCGTCTATT	TCAAGTCTTC	AAAGTGGATG	TTCTCATTTN	CCATGAATT	CAGTTTCTCN	180
GCCATATTCC	ACGCTTCTACA	GNNGGACATT	TAATTTTNC	CACCTTTTC	AGTTTTCTC	240
GCCATAATTTC	ACGCTCTAAA	ATGTGTTATT	CTCGTTTNCC	GTGATTTC	TTTTCTCGC	300
CAGATTCAGG	GTCCTATAAT	GTGCGTATTCT	CATTNNNCAC	GTTTTCAGT	GATTTCTGCA	360
TTTTTCAG	TGCGAACG	GATGTTTCTC	ATTTCMCATG	TTTNCAGT	TTCTTGNAAT	420
ATTCATGTC	CTACATACTGAT	CATTTTTAAAT	TTTCCACCTT	TTTCATTTTC	CACGCCATAT	480
TTCATGTCCT	AAAGTGTATA	TTTCTCTT	TCGGGATT	TCAGTTTCT	CGCCATATTC	540
CAAGGCTTCA	ACTGTTCTAC	CTCTCATTTT	CACCTTTTC	ACTGATTTCG	TCATTTTTCA	600
AGTCGTCAC	TGGATCTTC	TAATTTTCCA	TGATTTTCAG	TTATCTTGT	ATATTCATG	660
TCTCTAACGTO	GACATTTCTA	AAATTTCCTA	CTTTTCACAT	TTTCTCGAC	ATATTGACG	720
TGCTAAAGTG	TGTAATTCTT	TTTTTCCTG	ATTTTCAGT	TTCTGCCCC	ATTCAGGTC	780
CTAATAGTGT	GTATTTCTCA	TTTTTCACCT	TTTCAGTGA	TTTCGTCTT	TTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	GTGCACTT	CTTGCATAT	TCCATGTCCT	900
ACAGTGACAT	TCTTAAATAT	TATACCTTT	TCAGTTTTC	TCACCATAT	TCACGTCCTA	960
AAACTATATA	TCTCTCATTT	CCCTGATT	CAGTTTCCCT	CCCATATTCC	AGGTCCTAC	1020
GTGTGCAATT	CTCATTTTC	ACGTTTCTCA	GTAAATTCTT	CATTTTTAA	CCCTCAAT	1080
GGATGTTCT	CATTTCCTAT	GATTTTCAGT	TTTCTGCGCA	TATACCAATGT	CCTACAGTGG	1140
ACATTTCCTAA	ATTATTCACC	TTTTTCAGT	TTTCATCGG	ACATTTCAAG	TCCTAAAGTG	1200
TGTATTCTCA	ATTTCAGT	ATTTCAGT	TTCTCGCCAT	ATTCAGGAC	TCACAGTGTG	1260
CATTCTCAT	TTTCACGTT	TTTCAGTGA	TTC			1293

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (iii) MOLECULE TYPE: Genomic DNA
- (iv) HYPOTHETICAL: NO
- (v) ANTISENSE: NO
- (vi) FRAGMENT TYPE:
- (vii) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAACT	AGACAGAAGG	ATTCTCAGAA	60
TCTTAAATTGT	GATGTCGCC	CCTCAACTAA	CAGTGTGAA	GCTTTCTTT	GATAGAGCAG	120
TTTGAAACAA	CTCTTTTGT	AAATATCGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTC	180
CGTTGGAAAC	GGGATTTGCT	TCATATAAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTTT	CACTTGAACT	CACTGTTG	AAACAGTCCC	TTTCATAGAG	CAGGTTTGA	300
ACACTCTT	TGTGAGTATC	TGGAAATGGA	CATTGGGAGC	GATCTCAGGA	CTGGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CCTTGGAGAG	AGCAGTTTG	AAACACTCTT	480
TTTGTGGATA	CTGCAAGTGG	ATATTGCT	AGCTTGTGAG	TTTCTGTTGG	GAAACGGGAT	540
TACATATAAA	AAAGCACAGC	CAAGCTTCCC	AGAAACATTG	TTGTGATTT	TGCAATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTGAA	ACACACTTT	TGATGTATCT	660
GGATGIGGAC	ATTCGAGG	CTTTCAGGCC	TAAGGTGAA	AGGAATATC	TCCTCCCTGAA	720

AACATAGACAG	AAGCATTCTC	AGAAACTTAT	TTTGATGATG	GCGCCCTCAAC	TAACAGTGT	780
GAAGCTTCT	TTTGATAGAG	GCAGTTTGA	AAACACTCTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGCTAG	CCTTGGAGAT	TTCTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900
CATTCCAGA	ATCTTGTTG	TGATGTTGC	AACTCAAGTC	CAGAGTTGAA	CATTCCCTT	960
CAGAGACCA	GTTTGAACAC	TCTTTTATA	GTATCTGGAT	GTGGACATT	GGAGGGCTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCAGCTGG	GGGCTCTCAA	TCAGGCAGGG	GCCCCCTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAGG	GGGGTCAGGG	TGCATGAGT	GACACAGCTG	TAGGACTTAC	TGGGGGCTGT	120
GAGGCTCTGA	GGGGGGGAGA	AAAGCCCATG	AAAGTGCCTA	GAAGAGACAA	GTCGGCTGAA	180
GAGGGCTCTG	GGAACATAGA	GCTGGAGGAT	TTGGGGCTTG	GTCTCAAGCA	GGAAAGTGAAG	240
AAATGGGACAG	GGGTTGGAGAT	ACTCTACTCA	GTAGCAGGAG	GCTCTGGGT	CCCAGGACAT	300
TGCTTATCTCTG	GGGGTTCACCC	CCCCAGTTTG	AAGGCCCTGG	GGGGAGATGGT	ATGCCAAGAG	360
ATTACAACTGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAACCC	TCAAATCCAA	420
AGACCATGAG	TAGGGGTGTC	CACTGCAGCC	CTCTGACTGA	GTGTCATTGT	AGCAGCTTCA	480
AGGGCCCTG	CTGGGCTGTC	CTGGCTCATG	GCATCCACAT	GACCCCTGGC	CAACCCGTT	540
TAGGGTCTCTG	CTGAAAGACCA	AGATCCCTGT	TATCATTGAC	GACTCTAAA	TGAGCAGAGA	600
TTTCACCTCA	TTCGAAACAA	TCACAAAAAA	TCCATCTCTG	AAAAGGCTTG	GGGGATGGCA	660
CTAAAGCTAC	GGTAGGGGTG	GGATGAAGAT	TATAGTTACA	GTAAAGGGTT	TAGGGTTAGG	720
GATCAACCTT	GGTTAGGAGT	TAGGGTACAC	GTAGGGTACCC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGTTA	GGGTTAGGGT	TAGGGTTAGG	TTAGGGTTA	GGGGTTAGGG	TTAGGGTTA	840
GGGTAGGTG	TTGGGTTGGC	GTATTTTGTG	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGCTTCTG	TTTTCTTC	AGCAATTGTC	CATTTTAAA	AGAGTTTACG	AACTCTAAC	960
GATATAGACCC	AGCTGTGCTA	ICTCATGTG	GTTCATCAATT	GTAAACACAT	TCTGGTTCTA	1020
ATGTGTTTAC	TTGCTCATCTG	TAGATCTCTC	TTGGGTGAGG	GTGCTGTTCA	GATGTGTTG	1080
CATTCTCTGN	NTTITNGCTG	TTTAACTTAT	TTTTAGTTT	TAATAATT	TTATATATT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTTATTC	CAATAATTTC	TCATAATATG	GCTTCTCTT	1200
TGCTCTAAC	AAAGTCCTT	CAGAGAACAC	TTAAATATA	GAATCCACA	CTGTCACCTC	1260
TTTGTGTTAT	ATCTCACCTT	TGTGTCATT	GTAAATTCAT	ATTACCAAAAC	CCAAAGGCG	1320
ATAGCTTTC	TTCTATGTT	TCTCTGAA	ATTGTTATAG	TTTGCATT	TTAGTGTAA	1380
GATGATTGTT	AGTGATTATT	TGTGTAAGT	GTAAAGTTT	CGTCATATAC	CATATCATTT	1440
CTTATGGTT	CCAAATTAATC	TGTCCTCTAC	TATTTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTGAG	TAGATAGGT	GCTAGACATG	AAACAGGAGG	GGCCTCTGG	AAAGGGAAA	1560
GTCCTGGAAAG	GCTCACCTGG	AGGACCCACCA	AAAAATCACA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGATGGA	TGGGCACTTG	TCAATTGTGG	GTAGGGAGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCTC	TGAAGATGCC	CCAAATCATTC	ACTCTGCCAT	AAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGAC	TCTTAAAGTG	AAACCTGGCA	1800
CCATAAGTC	AGATTAAGGGC	AGAGAAAGGC	ATTCAAAAGA	GGCAGGGCGCA	GTAGGTACAA	1860
ACGTGATGCG	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GTCTGGTGC	GAGTGGATTG	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGGAGG	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTGGG	GGAGCTAAGG	CAGTAGCAGG	AAACAGCAGC	AAAGAAAAAC	GGTGGAGACT	2040
TGAGACAGAG	GGCAGGAATGT	GAAGAAAATCC	AAAAATAAAT	TCTCTGCACA	GAACCTTTAG	2100
GCTGTGTTAT	GCATCCTCA	GTCCCTCACTT	TCCTCTATT	TCTCAAAATA	ACTCTTTTACA	2160
CTGTTGTTCT	TTTCAATGAA	TGTTATCTGC	ATCTTGTAT	TCGCTCTTG	TGAAATGTG	2220
CTTCTCAAGT	TAACAAAGAA	CTGGGACATC	AGCTCTCCC	AGTAATAGCT	CGGTTTCAGT	2280
TTGAATTTCAC	AGAACCTGATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAAGGAGG	2340

CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG	2400
CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTAGC	2460
ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG	2492

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGAATTCA TTGGGATGTT TCAGTTGA

28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAACGCTC TCGCACC

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...942

(D) OTHER INFORMATION: Renilla Reiniformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg 1 5 10 15	48
ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val 20 25 30	96
CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn 35 40 45	144
GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg 50 55 60	192
CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp 65 70 75 80	240
CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg 85 90 95	288
TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile 100 105 110	336
TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu 115 120 125	384
GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val 130 135 140	432
CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro 145 150 155 160	480
GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys 165 170 175	528
ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys 180 185 190	576
ATC ATG AGA AAG TTA GAA CCA GAA TTT GCA GCA TAT CTT GAA CCA	624

Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro 195 200 205	
TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg 210 215 220	672
GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val 225 230 235 240	720
AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met 245 250	768
TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly 260 265 270	816
GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTC AAA GGT CTT CAT Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His 275 280 285	864
TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser 290 295 300	912
TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA Phe Val Glu Arg Val Leu Lys Asn Glu Gln 305 310	945

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTCTA TGTACAGGAT GCAACTCCCTG

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTAC

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTTCCACCGCA CGTTGTCATA	TGTAGATGAT	AATCATTATC	AGAGCACCGT	TGGGGATAAA	60
TGTCGACATT	TCCACTCCA	ATGACGGTGA	TGTTATAATGC	TCAAGTATIC	120
TTTACCACTAA	CTAGGAACTG	GGTTTGGCCT	TAATTACACTT	TCTCTGTTTT	180
AGGTCGACAG	GACTGCACC	ATTAAACATT	TGTCAGGCC	CTGTCCTGGAC	240
AACAGGCCCTC	AGCTTAATGTC	AAGATACAGA	GAGGCTCTCAT	ATGJGACTACA	300
ATCTTGTCGA	GATACAACTA	GATGTATTAT	GCAAAATAAC	GTCACTATAG	360
AGTTTCCGGG	ATTTGTTGTT	ATTTCCATTG	AGTATGTTAA	TTTACTTACGG	420
TGTCAAAACG	TCTTTTCAG	TATATGTTAC	AGAATTTGGAT	ACAGCTAATT	480
TTTCGGGAATT	GAGACTTCAG	TCGAACCTCA	GGCGCTTGGG	GCGTGAATT	540
TACCAAATTC	GATCTCTCTCA	GCATTTCTCT	TCTTTAAAAA	GAACAGATCC	600
TTGGAGATAC	ATCTTGTGT	GGATTAGTGT	ATGGTTGGGA	TTAATATTAT	660
CCCCAAACTAG	GAGAGAACAG	GTGTTTATTG	CCCAGGGCGT	AACTTTAAGG	720
TCTCCCTCTGA	TATATGGTTA	TCTATGCTTA	GGCAATTAAGGT	TGCAAGACTA	780
TATCCCACCA	GGCTAGTCTC	ATTGTACCGG	ATAGAGTGAG	CGCTGCTTCAG	840
GAGTGTCAAG	GCTAAGACACT	GCATGGAAA	GGCTCTCGGG	CAGCCCGAGA	900
GGGGACATGT	CATTTCTCAT	GAAGGTCAG	TCTGCTTAGTT	CATATATGTC	960
ACATCGGGAG	AGGTGCAAGGT	TGCTCTGGGT	AAAAGCTGT	CCCTTCCCC	1020
TACATGGCTC	TTTACCTCAT	ACACTGGGG	TGGGGCTGGGA	AGGCAAAACG	1080
GGGTGGCTCA	TTTACCTCTTA	TTAAAGGGAA	AGGGGGAGAT	GCTAATCTCG	1140
TGCGCGTTAC	AAGATGGGCC	TGACAGCTGT	GTGCTTAAGTG	GGCCGCCACAT	1200
TGTGCGGAGG	GTGTTTCTCTC	ACTCTCATGT	CTCTGCTCTC	GTAAACAAAT	1260
GATGGGGCTCT	GGCAACATCAG	GGAGTGCAC	CCCGCTGACGT	AACTCTGGCC	1320
GGGACGGGGT	TTCTCTCTCT	TGCTTCTCTC	AAGGGAAATT	CTCTCTTAATA	1380
GCTTCCCGTA	AAAGTGATAAT	GATTATCATC	TACATATCAC	AAACGTGCGTG	1434

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACCGCA CGTTGTCATA	TGTAGATGAT	AATCATTATC	AGAGCACCGT	TGGGGATAAA	60
TGTCGACATT	TCCACTCCA	ATGACGGTGA	TGTTATAATGC	TCAAGTATTTC	120
TTTACCACTAA	CTAGGAACTG	GGTTTGGCCT	TAATTACAGAC	TCTCTGTT	180
AGGTCGACAT	ACAACATAGAT	GTATATTGAC	AAATAACTCA	GTAGGGATGT	240

TTCGGGGATT	GCGTGTATT	TCCATCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTGT	300
CAAAAAGTCT	TTTCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTGAA	CAGATCCITC	360
GGGAAATTGAG	ACTTCAGGT	AACCTCACCG	GCTTGGACCT	GTCCCTGACC	AAAGGATTAC	420
CCAACTGGAT	CTCTCAGCA	TTTCTTCT	TTAAAAAAATG	GTTGGGATTA	ATATTATTTG	480
GAGATTAACAT	TTGAGTGGG	TTAGTGTGTC	TTCTTGTGATT	GTCCTGTAAG	CTTAAGGCC	540
AAACTTAGGAG	AGACAAGGTG	TGTTATTGCC	AGGCCGTTGC	AGGACTAGAA	CATGGAGCTT	600
CCCCCTGATAT	ATCTATGCTT	AGGCAATAGG	TGCGCTGGCCA	CTCAGCTCTT	ATATCCCATG	660
AGGGTAGTCT	CATTGACCGG	GATAAGTGTG	GTGTCGCTCA	GCAGCCGAG	AGAGTTGQAC	720
GGCTAACGAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	780
TCACTTCTCA	AGAAAGGTGGA	GTGTCCTAACG	GTCTCTTCTC	CAGGCAAAC	GACACGGGAG	840
CAGGTCAAGG	TTGCTCTGGG	TTAAAGGCTG	TGAGCCTAAC	AGCTTAATCC	FATCATGGCT	900
CTCTTACCTA	CACACTGGG	ATTGACCTC	TATCTCCACT	CTCAATTAAATA	TGGGIGGCCT	960
ATTGTCCTT	ATTTAAAGGA	AAGGGGAGA	GTGTTGGAGC	CGGGCCACCA	TTCGGCGTTA	1020
CAAGATGGCG	CTGACAGCTG	TGTTCTAAGT	GGTAAACAAA	TAATCTGC	ATGCGCCGAG	1080
GGGGGTTCTT	CATTCCTATG	GCTCTGCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
CAGTCATCA	GGGAGTGACA	CGTCTAGGGC	GAAGGAAATA	TCCTCTTAAT	AGGGGACGGGG	1200
TTTCGTTTCT	TCTCTCTCTT	GCTCTGCTCT	CTCTTGTTC	TGCTCTCTT	TTCTGAAAGA	1260
TGTAAGAATA	AAGCTTGTCC	CGAGAACGATT	CTGGCTGTG	GTGTTCTCC	TGGCGGTGCG	1320
TGAGAACCGG	TCTAACAAAC	ATTGGTCCCG	AAACCCGGGT	GATAATGATT	ATCATCTACAA	1380
TATCACAAACG	TGGCTGGAGG					1400

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTCCACGCA	CGTTGTGATA	TGAGATGAT	AATCATTATC	ACTTTACGGG	TCTTTCACT	60
ACAATCGGCA	CGAGGGCCCG	TGCTCTGGTA	ATAGATCTT	GTGTAAGAAGG	CAACACATG	120
ACACATTACT	CAAGGTGGG	TCTATCTGAGC	TGCGAGATCA	GCTTAATATG	AACTTGTCCA	180
ATTGTTGTGA	ATCATTAATAC	TTCAAAAGTG	CACTTCATGC	CAGACACAGG	TGCCCACCTT	240
TGGCTATAAT	AAACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTGTAG	300
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTGAGAGCT	TAATTTAAAT	AAAGTGTAT	360
ACCTTAATAA	AAATTTAAATA	AGAAGGTGTC	AAATATAC	AGTAGGTTAA	TTATTTCATT	420
AAATTATTTT	CTTCTTATAT	TTCTTAAAT	GTGTTCTGCT	ATGTCATT	GCACATCCAT	480
ATGTCATTAT	CTTCAGCTGTA	ATGAGAATAA	GTAGAAATAA	TACTTTCGGA	ACAAGITGTA	540
TCAAAATATGT	TACACTGTGAT	CCCTGTGTT	ATCTTACATT	TTATTTATTAT	ATGATTGTCA	600
TTCCCTCTGT	ACTTGTGAT	ATTACAAAGGT	ACATATTTAT	TCTCTCAGAT	CTTCATTATA	660
CTCTAACCAT	TTTGTATACAT	ACTTTATTA	TTCTTCTCTT	ATGTTGCTG	TGAGGCACAA	720
ATGCGAGAGA	GAACATTGAGC	AGATAAGAGG	ACAATTGCA	AGAGTCAGT	ACCTCTGTG	780
GTTCCTTGG	AACTCAGGAT	CAAAATTCTGG	TTGTCAGGCT	TGGCAGCATG	CACTTTTTCAC	840
CAGTCCTTCC	ATCTTGTAG	CCCTGAACAT	CAAGCTTGC	AGACAGACAG	GCTACACTAA	900
GTGAACCTGGT	CATTACAGCAG	ATGCACTGGT	ATTTATGTT	ACTTTCTATT	CCATGCTTT	960
ACTATTTCTA	CTAGGTGCTA	GCTAGTACTG	TATTTCTGAGA	TAGAAAGTTAC	TGAAAGAAAA	1020
TTACATTGTG	TTCTTATGAGT	CTTGTGACTG	CTTTCAGCAG	ATATAGAGTT	TTAATCAGGT	1080
CCTAGACCC	TTCTTCACTC	TTATTAATA	CTAAGTACAA	ATTAAGTTA	TCCAAAACAG	1140
TACCGGATGT	GAATTTGTGC	AGTTCTACTA	TGATAATAGT	CTAGCTTCAT	AAATCTGACA	1200
CACTTATTTG	GAATGTGTT	GTAAATAAA	GATTCAAGGT	TTACTCTAGG	TCAAGAGAAT	1260
ATTAACACATC	AGTCCCAAT	TACAAACTC	AATAAAAGAT	TTGACTCTCC	AGTGGTGGCA	1320
ATATAAGTG	ATAATGATTA	TCATCTACAT	ATCACAACGT	CGCTGGAGG		1369

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22118 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCCCCT	ATCCCTAATC	CAGATTGGTG	GAATAACTTG	GTATAGATGT	TTGTGCA	TT	60
AAAAGCTTGT	AGGATCTTC	CTCTAGGCA	CTGGACCTG	AATTGTGGCC	120		
CTGAGTATA	GGTCCTGGGA	CATATCGAGT	CTGCACAGA	CAGACAGACA	180		
CACAGACAGA	GACAGACGGT	ACAAACAAAC	ACGTGAGGCC	GTGTGCCAAAC	240		
ACACCATCT	GGGCCATTA	ATTGAGGACG	TTGATTTAT	ATTCCTGTG	300		
TCTGCTGTC	TGCTGTGTC	TCTCAACAGCA	GAATATGATT	TGTAGCTG	360		
CCCTGCTGCC	TGCGCTGCTG	CCCTAACAGCA	AAAGAACCTT	AACAATTATG	420		
CCTCTCTAATG	TTGCTCTTTT	TCTCTCTCTT	TATCTTTTC	CTCAATCAA	480		
TCTCTCTTC	CTTCTCTCTC	TCTCTCTCTT	TTTTTTCTT	TCTTCTCTT	540		
TTCTTCTCT	CTTCTCTCTA	TTCTTCTCT	ACATAGTTTC	TTAGTGTAA	600		
TGCTTCTAAG	ACAGATTTGTA	GGCCATCAATC	CTGTAAGAGC	CATCCCTGAC	660		
CTGCGATGAA	TGTTGTACCT	CATCATGACC	AGCTTGTACT	CTTCCTCTGC	720		
AGGAGTTC	AGAAGACTGG	TTATATTTTT	CATTATAAT	CTAACGTTAA	780		
ATTTCACCAA	AAGAATTAG	ACTGACCAAAT	TCAGAGTCTG	CCGTTTAA	840		
AAAGTAGGAG	AAAACACCTG	GGCTGTCTGT	GGATGGTCTGA	GCTGCTTITA	900		
TCACCATCTT	GCACATGCA	ACCGGGCCAC	TAGAACCCG	GGGAGCCTCG	960		
ACCTGGAAAT	AATAGGTAC	TAAGGGCCA	GCCACCTTCA	TAAGGGAGA	1020		
GTTAGCAGAC	AGAGATGGCTC	CCATGACAT	GTGTTCTTTC	CGGGAGTTCA	1080		
CAACCGAGTC	ACAGAACAG	GAAGATATACA	CAGTGTGTC	GGTCAAGAGTIA	1140		
CAGAGAACAC	ACATCTTGA	AAAAACAAAAA	AAATAATTA	AGAGTTTACA	1200		
TTAAAGATAG	CCGGGAGTGT	TTGGGGATGT	CTTAAATCCC	ATTTAAAAT	1260		
GGGAGGATT	CTGAGTTGA	GGCCAGCTGT	GTCTGCAAG	AGCTCTCTTC	1320		
GCTATACAGA	GAACCCCTGT	CTTGAACAACT	AAACTAATT	AGGCGAGAT	1380		
ATATAAAAAT	AAAAATTTA	AAAAGATTTA	AAAAACTACA	GAACAGCTC	1440		
GAGATGGCA	GTAATGCTAA	TCATAGCAGA	AAATTATAC	ACACACACAC	1500		
TGTCATAAAA	CTTCAATGTA	CTTCATGATG	ATCAAATTC	GATAGTCAGT	1560		
GAATCATATA	TCTGAAATAA	AAAGCGGAAAG	CCTTTCTGTC	AAACTAAACT	1620		
AGATAGGTT	TCTCTCATG	TAATCTCTGC	ATCTCTGCCT	GGAACTTCC	1680		
GGTAGCTCTA	AACTCAGAGA	GGTCTGATG	GCTCTGCTG	TITGTGCCCCA	1740		
CTGCTGCTC	GGCTCTCTCA	CTTCTCTCTG	CACCCACACA	ACCTAGGATC	1800		
TTTATTTCT	TCTCTTCTC	TCTCTTCTCT	TTCTTCTTCTT	CTTCTTCTTCT	1860		
CTTCTTCTC	CTTCTTCTCA	ATTAGTTCT	AAATGTAATG	TGTTGTTGTG	1920		
TGCTCTATAGG	CCTGCTTGTG	AGGAGAGGGC	AAACAGAACCT	ACCATGCGAC	1980		
TCTCTGAGAAT	AAGTGGAAA	ACAAACAAAC	AAAGGAAATTC	AAATCACATA	2040		
ATATGCCAG	GCTGCTGAGA	TGCTTTTAA	GGCTTAGTGT	GAATGTGAT	2100		
TGCTTCTTAT	CCAAACACAG	AGAGAGGTTG	GCTCTGGCTGT	AAATGCTGTG	2160		
AGACGGACCT	GGCCCTTGAAC	ACATTAATCT	GTCCTGCTCT	GCTCTGCTCT	2220		
AAAGGCAATG	GCCCAACTGT	CCCGGGACTGA	TTCTTCTTCTT	TTTTTTTTT	2280		
CTTCTTCTCT	TTTCTCTCT	CTCTCTCTC	CTCTCTCTCT	TTCTTCTTAT	2340		
TTTCTTCTT	CTTCTTCTT	TTTTTTTAA	AAATTGCTTA	AGGTTAAAGG	2400		
AAATGCCCTCA	GCTCTGCTCT	AATTCTCTT	AAAAAAAAC	ATGATGCTCAC	2460		
CAGTATGAT	GTATGATAT	TTAGAAGAAA	TAATAATCCA	TTATAAACTC	2520		
AAATTCATGT	CATTCTGTG	CCACAAAGTG	AGTTCCAGGA	TTTACACAGAG	2580		
TTCAATTT	TGTTGTCAG	GTCACTCTG	CTTACAAAGT	GAGTTCCAAG	2640		
CTACACAGAA	AAACCATATC	TCAGAAAAAA	AAAAGTCCC	TCGATAGGG	2700		
ACACACACAC	ACACACACAC	ACACACACAC	AAACACACAC	CGCCGCCGCG	2760		
AAAGTGTGTC	AAAAATTAAT	ATTTTCTG	CCAAAGTGA	CGATGAGGGC	2820		
TACTCTAGA	AAAAATTAAT	ACAAACGGGC	TTTTAATCA	TATGAAGAGG	2880		
AACTCTGAAT	TTAGCTTGTG	AAAAGGGGC	TTCCAGCACT	GTGAGTAA	2940		
ACGGGGCAGG	GGGGGGGTTA	GGGTGTGGGT	GAGTGAGGGC	GAGGGAGCAG	3000		
ACCCCGAGGG	TTAGAGTGT	TTAAAAATGA	GACCTTAATG	TGGTGGAAAG	3060		
CCACCTCTCT	CTTCCACTGC	TTAGATGTC	CCCTCCCTT	GAGGTCGCG	3120		
CTGCTCTAA	CTGCTCTGT	TCCTCACCC	CCGCTGATTG	ACTTTGACTT	3180		

CAAGAACGAT	TTTGCCTGTT	TTCACCGCTC	CTGTCTACAT	TTTCGTTTTT	GGGTGCCCGA	3240
GTCCTAGCCG	TTCGCTATGT	TCGGCGGGG	CGATGGGGAC	CTTGTGTGCG	ACTCGGGAGA	3300
AGTGGTGGGT	GGGTGACGTC	CTCCGCTG	TCGGCGTGAG	TGCCGGAAAC	TGAGCTCGGG	3360
AGACCCCTCG	GAGAGACAGA	ATGAGTGAGT	GAATGTGGG	GCCGCTGAGC	GATCTGTATT	3420
GGTTGTATG	GTGATGTCGAG	ACCATGTCG	GCGGACACTT	AGTGGTGACA	AGTTTCGGGA	3480
ACGCTTCAGG	CTCTCTCAGGT	TGGTGACACA	GAGAGGGAA	TGGCTGTGCG	TGAGGCCGAC	3540
AGGGTACAGC	GAGGCCGCGG	AACGAGCGG	GAGCGCTCG	GAGATGGTGT	CCTGTTAAAG	3600
GACCGTCTCT	AAACAAGGAGG	TCTGACAGGG	AGATGGCCAA	AGCACCGGA	GTGCTGTGAC	3660
GCCCCTTGG	GAAAATGCT	AGGGTGGTGT	CGAACCTTAC	TAAGGTGAGC	AGAAAGGCTTA	3720
AGTCCTACCC	CCCCCCCCCT	TTTTTTTTTT	TTTCTCTTAC	AAAGCCCTTC	TTGTCCCCGT	3780
CACGGGGGGC	ACCGTACATC	TGAGGCCAG	AGGACCGAT	GGGCCGGCT	TCCAAGCCG	3840
TGTCGCTCGC	CTTCGCTGGC	TTGGGCTCT	TTTTTTTTTT	TTTTCTCTCA	3900	
GAAGCCTTGT	CTGTCGCTGT	CAACGGGGC	GCTGTACTTC	TGAGGCCAG	AGGACCGAT	3960
GGGGCCGGGC	TTCCGACCGC	GTCGCTGGC	GCCGCTGAGGA	GCTTCGGTC	TTTTTTTTT	4020
TTTTTTTTT	TTTTTTCTC	CAACAGCTT	GTGCTGCGT	GGCCGCTG	GGCCGCTACT	4080
TCTGAGGCCG	AGAGGCCGCG	ATGGTGCGC	TTCAACAGCG	ATGTGGCGGG	GCCAGCTGGA	4140
GCTTCGGGT	TTTTTTTTC	CTCTCAGA	CTCTCTTGT	CCCTCGCACC	GGGGCCGCTG	4200
TACTCTGAG	GCCGAGAGGA	CGTGATGGC	CCGGGTCTCA	GCGCGATGTC	GCCCGGGTCAG	4260
CTGGAGCTT	GGATCTTGT	TTTTTTTTTT	CTTCAGAAGA	CCCTCTCTTG	TCCCCCTCAG	4320
CGGGGGGACC	TTTACATCTG	GGGGCAGAGG	ACGTGATGGG	TGGCGCTTCC	AAAGCCGATGT	4380
GGGGGGGCCA	GTCGCTGGCT	GGGGGAGAGG	GGGGGAGAGG	CAAGAGCCCT	CTCTTGTCCC	4440
CGTACCGGG	GGGGCTGTAC	CGGGGTTTTT	TTTTCTCTC	AGAGGCCCCG	GTTTCCAGGC	4500
GGATGGTCCG	CGGTGCTCGT	GACCTTGGGA	TCATTTTTTT	TTTCTCTCTC	AGAAGCCCTC	4560
TCTTGTCTCC	TCGACCGGGG	GGACCGTACA	TCCTGAGGCC	AGAGGACACG	ATGGGCTGT	4620
CTTCCAAGCC	GATGTGCCCC	GGCCAGCTGT	AGCTTGTGCT	CTTTTTTTTT	TTTTTCTCTC	4680
CAAGAACGCTT	TCGACGGCTG	TCGACCGGGG	GGCGCTGTACT	TCCTGAGGCC	AGAGGACGCG	4740
ATGGGGCCGG	CTTCAGAAC	GGTGTGGCTC	GGCCAGCTGG	AGCTTGGGGT	CTTTTTTTTT	4800
TTTTTTTTT	TTTCAGGAGA	AACTCTGTCT	GTGCTGTCA	CCGGGGGGCG	TTGTACTCT	4860
GATGCCGAGA	GGAGGCCGATG	GGGGCGCTT	CCAGGGCGAT	GTGGCCGGT	CAGCTGGAGC	4920
TTTGGATCTT	TTTTCTCTCA	GAAGGCTCTT	TCATTTTTTT	CTTGTCCCCG	TCACCGGGGG	4980
CACCTTACAT	TCGAGGCTCA	GAGGACAGCA	TCAGGGGGGG	TCAGGGCC	ATGTGGCCCG	5040
GTCACTGTA	GCTTGGTATC	GGGGCAGAGA	GGACATTATG	GGGCCGGCTT	CTAACCTGGAT	5100
GGTGGCTGCA	GGGGGGGG	TTTGGATCTA	ATTTTTTTTT	TAATTTTTTC	TTCCAGAACG	5160
GGTGGCCCGT	CAGCTGGAGC	GGGGGGGG	CACTCTGGAC	CGAGAGGACA	TTATGGGCC	5220
CCTCTTGTCC	CTGTCACCGG	GGGGGGGG	GGGGCTTGG	GGCTGTACT	TTCCCTCTCG	5280
GGGCTTCAGG	CCGATGTTGG	CCGGTCAGCT	GGAGCTTGG	ATCTTTTTT	TTTTTTTTCT	5340
TTTTCTCTCA	AGAAGGCCCTC	TCGTGCTCTG	TCACCGGGGG	CCCTGTACGT	CTGAGGCCGA	5400
GGGAAAGCTA	TTGGCGGGT	TTTCTTCTCA	TCACGGGGGG	GTCTTATCAG	TTCTCGGGGT	5460
TGTCAGGGTC	GACCACTGTG	TTGGGATCTA	GGGGCTTGG	TTCTGTATGG	GGTCATTTT	5520
GGGCCAACCTC	GGGGGGGG	TTCTTCTGAGG	TCGGGGCTCTT	GGCTGTACT	TTCCCTCTCG	5580
TCTCTTATG	GCTGTGTATC	TTCTCTATCT	GTTCCTATTG	GGCTGGAGGA	TAGGTACTGA	5640
CACGCTGTCC	TTCTCTTAT	AACTAACAAAG	GACACTATAA	AGAGGACCTT	TCGATTTAAC	5700
GCTGTTTGC	TTGTCAGCC	TATTCCTTTT	ACTGGCTTGG	GTCTGTGCGG	GTGCCCTGAAG	5760
CTGTCGGCGA	GCCACGCTTC	CTGCTTCTCC	GGGGCTTCTG	CTTCGGCTGT	CTTCGGCTGTG	5820
GCAGCTGTG	AAACAGTGGC	GCCTGTGACTT	TCCTGCGTGT	CAGACGTTT	TCCCCTATTTC	5880
CCCGAGGTG	CGTGTGTCACA	CCCTGGGGG	TTGGAAATGG	GGAGGCCAGT	GTGGTTGAGG	5940
GCCACCTTAT	TTCCGGCTAC	TTTTTTTTT	TTCTCTCTC	TTGAGTCCC	GAACCTCCGC	6000
TCTCTTCTCT	TCCGGCTCTT	TCTCCACAT	GGCTCCCGAG	TGCACTTCTT	TTGTTTTTTT	6060
TTCTCTTCT	TTGGGGAGGT	GGAGAGTCCC	GGAGAGTCCC	GAGTACTTC	CTCTGCTCTG	6120
TGGTGTGCAA	GTGTGTCATG	CACTGGCTTC	CCGGAGTGCAC	TTTTTTTTGT	GGCAGATCGCT	6180
CGTGTGTTTC	TCTGTTCTG	TCTGCTGCG	TATCAGTAAC	TGTCCTGCCC	CGGGCTGTAAAG	6240
ACATTCTAT	CTCGCTTGT	TCTCCGATT	GGCGCGTGT	GTCCTACTCTT	AGATCGATGT	6300
GGTGTCTCGG	AGTGTCTCTC	GGGGGGGG	CAAGGCCGGC	CGGGCGAGGG	ACCGACATTC	6360
ATGGCGAATG	GGCGCCGCTC	TTCTCGTCT	GGCAGCGGGC	CCTCGTCTCT	CCACCCCATC	6420
CGTCTGCCG	TGGTGTGTGC	AAAGGAGGGG	TGGCGCTCTC	CGGGCCCGACG	CTGCCCGGGG	6480
CGCACCTTTC	TCAGTGGTTC	GGCTGGTCT	TGTTGATGTC	TGAGGCCGCC	GGTTGTGCCC	6540
TCACGTGTT	CACTTTGGTC	GTGTCCTGCT	TGACCATGTT	CCAGAGATTC	GTGGAATGTG	6600
CGGGTGGCGT	TGCATACCT	TCCGGCTTGG	TGTTGTCAGC	CGCTGTTCT	TGTAAGCGTC	6660
GAGGTGGCTC	TGGAGCCTTC	CAGGTTTGT	TCTCTAGGTG	CTGCTTCTG	GTCTGGTGTG	6720
GCCTCTCCCA	TTCCCTGGTG	TGCTCTGGT	GCTCGTCTG	GCTGTGTC	TTCCCGTTTG	6780
TGTCAGGAA	GCCCGTGTAGA	GGGGGGTCTG	GGAGAGAAGG	AGGGGAAGA	CCCCCTCTTC	6840
CGTCTGGGGT	AGGGGGCCAC	CCCGCGACTA	GTACGCTCTG	CGCTGTGGCT	GGTGTGAGAC	6900
GGTCGGCGCT	GGGGTTGGAA	AGATTTCTGA	GAGACTCTA	GCTTTCTCGT	GGGGAGCTTT	6960
GAGAGGCCG	GCTTTTGGGG	GGGACCGGTT	GCAGGGTCTC	CCCTGTCCG	GGATGCTCG	7020
AATGCCCTTG	GAAGAGAAC	TTCTGTTG	CGCACGACCC	CCCGCGCGGT	CGCCCGCGGT	7080

TTGGTCTTC	GGTTTCCCTG	TGTGCTCGTC	GCATGCATCC	TCTCTCGGTG	GCCGGGGCTC	7140
GTCGGGGTT	TGGGTCGTC	CCGCCCTCAG	TGAGAAAGTT	TCTCTCTCTA	GCTATCTTC	7200
GGAAAGGGTG	CGGGGCTCT	ACGGTCTCGA	GGGGTCTCTC	CCGAATGGTC	CCCTGGAGG	7260
CTCGCCCTCT	GAGCCCTCC	CGCGCGCGCA	GGCTTCTGCTC	TCTCTCTAC	CGCGGCCCGC	7320
GGCTCTCCCG	CTCCGAGTTC	GGGGAGGGAT	CACGGCGGGC	AGAGCGCTGTC	TGTCGCTCTG	7380
CCGTGTCG	GGAGCATGTC	GCTCGCTTGT	TGTGGTGTGT	GCTCTGGGAG	AGGGCTCCGT	7440
GCACACCCCC	GCGCTCGGT	ACCTTCTCTC	CCCTCTGAGG	CCCGCGGTG	GGACGGGGTG	7500
TGGTAGGCG	ACGGTGGGT	CCCGGGTCCC	CACCCCTCTT	CCCGTCTCTC	ACCGTGTCT	7560
TCCGTCGCGT	GGCTCCCTCT	CGCTCGGGTC	CGAGACTTTC	CCGGCTCTCC	CGACGGCGGC	7620
CTGGGCCCGC	CGTGGTGCCT	GCTGTGTGCT	TCTCGGGCTG	TGTGGTGTG	TGCGCTCGCC	7680
CCCCCTCTCC	CGCGCAGCG	TTCCCACGGC	TGCCGAAATC	CGGGGAGTCC	TCTTCCCT	7740
CCCTGGGTG	GAGAGGGTCC	GTGTCCTGCGC	TIGATIGATC	TGCGCTCTCG	GGACGGGACC	7800
GTTCTGTG	AAAGACGCTG	TTGGCCCGT	CGCGCGCGAC	TCGCGACGTG	GGGACCCACT	7860
GCCACACCCC	GGCTCTCGTC	GGTAGGACATC	GGTGTGTCGG	CATCGCTCTC	TCTCTGTGT	7920
CGGTGTCGCC	TCCCTGGCT	CGCCGGGGC	CGTCGTTT	CGCGTCTCGT	CGCGCTGCA	7980
GGTGTGGT	GACTGTCAG	GGGGAGTGTG	CACTGTGATT	CCGGCGGTTT	TGCGCTCGG	8040
TGCGCTGACC	GGTCGCGACG	CGCAGCGTC	TCTCGGGCTC	TGTGAGGAC	CCCCCTCCGG	8100
GAGGGGCCCG	TTTCGGCCGC	CTTGTGCGTC	GTGCGCGGCC	CTGCTTCTG	TGTTGCTGTT	8160
CCCCCTCCCC	GTCGCGCGCA	GGCGCTTCTT	TTTCTCTCT	CCCCCTCTCT	CTCTCTACTG	8220
ACCCGTCGCC	GTGCTGTCG	AACCCCGCGA	TGGGGGGCGC	CGGGCACTGA	CGCGCTCGGG	8280
CGGTGACCGG	GGTGTGGGGG	GGGGGGCGAC	GGTAGAAGAAA	GTGCGCTTCG	CGGGCGGGAG	8340
GAGCTGTG	CGTGGCGAGG	TTGGAGGGCG	CCCCGGAGG	CGCTGCTCTG	CGGGCTCTG	8400
AGATGGTATT	CGTGGCGAGG	AAAAAGGGTG	CCCCGGAGG	CGAAAGGGAA	AGAGGGCTACG	8460
CCGGCCCTGT	CGTGGCGAGG	GGAAAGGGCG	GTGTTGGCT	GGTGGCTCTG	GGGGGCTCTG	8520
ACCCGTCAT	GGGGGGGGGG	TGGGGGGGGG	GTGTTGGCT	GGGGGGCTCT	GGGGGCTCTG	8580
GATGTCCTAC	TCCCTCTCCC	CGAGGTCTCA	GGCTCTCTCC	GGCCGGCTC	TGCGCCCTCC	8700
CCTCTGTCG	CCCTCTCGGC	GGGGTCTCAAGT	CGCTCTCGA	CTCCTCTCTC	TCCGCTCTTC	8760
CATCTCTCGG	CGCATGCGG	CGCCGGAGGT	CGACGGTGGT	TCTCTCTCG	CTCCGCTCTC	8820
TCGCCGGGG	CTGGCGCTCT	CCCGGGGAC	CTCTGGGAC	CCCCGGTTGG	GTGTTCTCT	8880
CTCGCCGGCT	TCGGCGACT	TCGCTCTCG	CGCGAGGGTC	AGGGGGCTTC	CCGTTTCCCC	8940
GACGCTTGGC	CTGGCTCTG	TGTGCTTGGG	GGGGGGCCCG	TGCGGCCCTC	GGCCGCCCGT	9000
GAGCCCCGGC	CGCACCGCCG	GGGGTGGCGGT	TGCGCGCGC	GGTCAGTTGC	GGCTCTGGGT	9060
TGTGTCGCGT	CGGGAGGCGT	TCCGGCTCTG	GGGGCGTAGA	CGGGGGTGTG	GGCGGGCTCC	9120
GACGGCTGG	CTATCCAGG	CTCCCCCGCG	CGCACCCCG	CTCGGGCGTC	CGCGTGTG	9180
TCGTTGGTGT	GGGGAGGTGAA	TGGTGTCTACC	GGTCATTCTCC	TCCCGCGTGG	TTTGACTGTC	9240
TCGCCGGTGT	CGCGCTCTC	TTTCGCGAAA	CCCCCACCGC	AACCCACAC	CCTGCTCTCC	9300
CGGGCGGGT	CGTCGCGACT	TCCGGCTCTC	CGCATGCGG	GGGTTGCTGGG	ATTGTCGCG	9360
GGGGAGGAGG	GGAGAGGGCG	TAAGAGGAGT	GTGCGAGAGC	TGTCGGGGGG	CGACGCTCTGG	9420
TGTTGGTTG	CGCGCTGGGT	GTGTCCTCGG	ACGGGTTTGC	TCCGACCCCC	ACGGGGTGG	9480
TCCCGCCGCA	TCGACTCTCC	CGTGGCGCCG	GAGCGGCCCG	CGCGCTCACG	CCCCGGTTTGT	9540
CCTGGCTCG	GGGCTCTCGG	TCCCAACCCC	TCTCTCTCT	CTCTCGGGCT	CTCTGTCCCC	9600
GGTGTGAT	GGGGGGGGGG	GGGGGGGGGG	TCGGGCTTC	TACACTCTGT	GATCCCTGGCA	9660
AGATGAAACTG	CGAATGGCTC	AAGATTAAGC	CGATCATGTC	TAAGTACGCA	CGGGCGGTAC	9720
CTACTTGGAT	AACTTGTGTA	ATTAATACAG	TTATGGTTC	TTTGGTGTG	CGCTCTCTCT	9780
TCCCCGGGG	GGATGCGTGA	ATTATTCAGA	TAATATCATG	CGACGGGGCGC	TGACCCCCCT	9840
CTCCGGCCG	GGGTGGCGGG	CCGGGGCGCTT	GGTGAACCTCA	GATAAACCTC	GGCCGATTCG	9960
ACGGCCCCCG	TGGCGCGAC	GACCCATTGC	AACCTCTGCC	CTATCAACTT	TCGATGTTAG	10020
TCGGCGTGT	TACCTGGTG	ACACGGGGTG	ACGGGGAACT	AGGGTTCTGAT	TCCGGAGAGG	10080
GAGCTCTGAGA	AACGGCTACC	ACATCCAAAG	AAGGCAGCAG	GGCCGGAAAT	TACCCACTCC	10140
CGACCGGGGG	AGGTAGTGTAC	GAAAAATAAC	AATACAGGAG	TCTTTGGAGG	CCCTGTAAATT	10200
GGAAATGAGTC	CACTTTAAAT	CTTAAACAGA	GGATCCATTG	GAGGGCAAGT	CTGTTGCCAG	10260
CAGCGCGGCT	AATTTCAGCT	CCAAATAGCG	ATATTAAGAT	TGCTGAGTT	AAAAGACTCG	10320
TAGTTGGATC	TTGGGAGGGG	CGGGGGCGGT	CGCGGGAGGAG	CGAGTCACCG	CCGGTCCCCG	10380
CCCCCTGGCT	CTCGGGCGCC	CCTCGATGCT	CTTAGCTGAC	TGTCGGCG	GGCCGGAAGC	10440
GTTTACTTTG	AAAAAAATTAG	AGTGTCAAAG	GCAGGGCGGA	GGCCGGCTTGG	TACCGCAGCT	10500
AGGAATAATG	GAATAGGACC	CGGGGTTCTAT	TGGTGTGTT	TTCCGAACTG	AGGCCATGTAT	10560
TAAGAGGGAC	GGCGCGGGGG	ATTCTGATTC	CGCGGCTAGA	GGTGAATTC	TTGGACCCGGC	10620
CGAAAGACGGA	CCAGAGCGGA	AGCATTTGCC	AAGAATGTTT	TCAATTATCA	AGAACGAAAG	10680
TCGGAGGTTC	GAAGACGATC	AGATACCGTC	GTAGTTCCGA	CCATAAACGGA	TGCGGACTCTG	10740
CGATGCGGGG	CGCTGTTATTC	CATGAGCTG	CGGGGGCGCTT	CCGGGGAAACCC	AAAGTCCTT	10800
GGTTCCGGGG	GGAGATGTGT	TGCAAGAGCTG	AAACTTAAG	GAATTCAGCG	AAGGGCACCA	10860
CCAGGAGTGG	GCCTGCGGCT	TAATTTGACT	CAACACGGGA	AACTTCACCC	GGCCCGGACCA	10920
CGGACAGGAT	TGACAGAATG	ATAGCTCTT	CTCGATTCGG	TGGGTGTG	TGCAATGCCG	10980

TTCTTAGTTG	GTGGAGCGAT	TTGTCGGTT	AATTCCGATA	ACGAACGAGA	CTCTGGCATG	11040
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GGCTTCAAGCC	ACCGGAGATT	GAGCAATAAC	AGGTCTGTGA	TGTCCTTAA	TGTCTGGGGC	11160
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GAATTCCTTAC	TAAGTGGGG	TCATAAAGCTT	CGCTTGAATTA	AGTCCTGTCC	CTTGTACAC	11340
ACCGCCCGTC	GCTACTACCC	ATTGGATGGT	TTAGTGAGGC	CCTCGGATCG	GCCCCCGCCCG	11400
GGTGGGCCCC	CCGCCCTTGC	GGAGCGCTGA	GAAGACGGTC	GAACCTTGACT	ATCTAGAGGA	11460
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TCAACCTTC	CTCGCTCGG	TCAGACCTCG	CAACCCCTACC	GGGGCGCGG	CTGCTGCGG	11760
GGCTCTTCTG	TCTCTCCG	CCGGCTCTTC	CGTGTCTAAC	AGGGGGGGTAA	CGTCGTTAG	11820
GGTTTTGAC	CCGCTCCGG	GGGGCTTCTG	CGTCGGGGCG	CGCCGTTTC	TCTCCGGCA	11880
CCCATCCCGC	CCGGCGCTCT	GGCTTCTCTA	CGTGTGCTGA	GGGGGGGGGG	CGGTGTTGGG	11940
GGATGTGAGT	GTGCGCTGTG	GGGCTCGCG	TCCCGATGCC	ACCTTTCT	GGCCTCGCT	12000
GTCCCTCCCC	CTCTCTGTC	GGGTGATCTAG	CTGTCGGGT	CCGGCGGGGA	GTTTAAAGGA	12060
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CGGTGTTGCG	GGCGCGCTC	CCTCAGACTC	CATGACCCCT	CTCCCGCCG	TGCCGCCGTT	12180
CCCCAGGGCG	GGGGCTGTG	GGGGGGGGGA	TGTCTGGAGC	CCCCCTGGGC	GGCGTGGGGG	12240
CCCCACCGG	GGCGCCGGCT	TGGCCGATT	CCCGGGGTGCG	GTCTGTCGG	TGCCGGTCTG	12300
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CATGACACT	TCGACACTAC	TTGACACTAC	GGGTTCCTCC	CGGGCGTACG	CTTGTGTCG	12660
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CTCGCAGGGG	ACCCCGCCCA	ACCGGCTCTG	GGCCCTCGGT	CTCCGAAAGT	TCAGACGTTG	12780
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GGCGGTGTC	GTCCTCTG	CGCCGCGCTC	CTCGCTCT	TCTTCCCG	GCTGGGGCG	13740
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GACGCTCATC	AGACCCCGA	AAAAGTGTG	TGTTGATATAG	ACAGCAGGAC	GGTGGCCATG	15540
GAAGTGGGAA	TCTGCTTAAC	AACTCACTG	CCGAATCAAC	TAGCCCTGAA	15600	
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CCCCATGGG	CGAACGTACC	ATCTGTGGGA	TTATGACTGA	ACGCCCTAA	GTCAAGATCC	18120
CCCCAAGGGC	AACGATACGG	CGAGCCCGAA	GGAGGCTCTG	TTGGGCCCCG	ATAGCCGGT	18180
CCCCCTCCGT	CCCGCTCGC	GGGGTCCCC	CGTGGCCCC	GGGGGGCGG	GGGTCTCCCC	18240
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TGGCTCTGTC	GTCTGTTGTT	TGTTGCTGTT	CTTGTCTGCT	TGTTGCTGTT	CTTGTCTGCT	20700
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CCAGCTCTTC	CTGCGCTCTG	GAAGATGTAG	GTCTGCTATT	GGGAAAAGCA	TTTTTGAGA	21240
GATGTCGTAG	TGACCAAGAG	AGTTGGTAG	TGACAGGAG	CACCCAGATCT	CATTGTGGGT	21300
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CTTCACAGCAC	CTCCCCCTCC	CCACACACTGC	CTTCTCTCTCT	ATGTTTGGGT	GGGGCTGGGG	21960
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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGACACGC	TGTCTCTGG	CGACCTGTCG	TGGAGAGGT	TGGGCTCCG	GATGCGCGCG	60
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GGCCGAGGCC	GAACGGTGT	GTGTCGTTCC	CGCGCCCGG	GCCTCCCTCT	CGGGTGGCGG	900
CCCGCGTGTG	CGCGCTGGG	TCTCTGGAGG	GCTCTGGGT	GTGGGTTTC	AGCGGTGTTG	960
AGTGAGACGA	GACGAGACG	GCCCTCTCC	CGCGGGAAAG	GGGCGCCGCC	TGCTCTCGGT	1020
GAGGCCACGT	CCCTGCTCC	CTCTGGCGG	GGCGGGCGG	GGCGGTGAG	CGATCGCGGT	1080
GGGTTCTGGG	CGGTGTA	GTGCGCGG	CGCGCCGCG	AGGGCTGCGC	GTTCCTCCCTC	1140
CGACGGCTGC	TGTTGGGGT	GACTCTGGG	GGCTCTGGC	TCGGAGGGT	GGAGGTGGGT	1200
GGACGGGGGG	CGCTGGTGG	GTTCGCGCC	CGCGCGACC	GGCGGGGCC	CCGCTCTGAA	1260
CGCGAACGCT	CGAGGTGGCC	CGCGGCAAGGT	GTTCCTCTG	ACCGCAGGGC	CCCTCTCCCT	1320
CCCCAGGGCT	CCCTCGGCC	CTCTCGGG	CGCAGGAGGA	GGCGCTGGC	GTGGGGGGG	1380
GTGTGACCCA	CCCTCTGGT	AAAAAGCTT	CTCTAGCGGT	CTAGGAGGCC	TGCTCTGGGG	1440
GTACCGATC	CCCCCGGCC	CGCGCTCTG	CTCTGCCCT	TTATGGTAG	CGCTCGGT	1500
GGCGACCCG	CGCAGAGGAC	CTCTCGGCC	TTCCCTCTG	ACGGGGTTGG	GGGGGAGAAG	1560
CGAGGGTTG	CGCGCGACC	GGGTGCGGG	CGGAGTGGG	CGCTCTCCCT	ACTGTGGCCC	1620
CGGCCCTCCC	CTTCGGATC	GGGGGAGGAT	CCCCCGGGC	CGGGCCCGC	GCTCCACCC	1680
AGCGGGTTGG	GACGCGGCC	CGCGCGGGG	GTGGGTTGTC	GGCGCCCGC	CTCTGTCCTG	1740
CGCTGTGACCC	CTTCGGTCC	CGACTCGCT	CGTGGCGCC	CTCTGGCCG	AGTCGTGACC	1800
GGTGTGACCA	ACCGGGTTG	CGTGGCA	GGTGGGCC	GCTGGGCC	GGAAAAGCGT	1860
CCCCAGGTGG	GGCGCGGCCG	GTCTCCCGA	GGCGGACCGG	CTGGAGGAT	GGACGAGAAT	1920
CACGGACGAC	GGTGGTGGT	GGTGTGCGG	GGTGGTGG	GGTGGTGG	GGGGCCCCCG	1980
GTGGCGGGG	CGCGGGGTC	CGGAGGGCT	TCTCTGGCTG	CGGGTGTG	GGGGCCCCCG	2040
CCCAGGCAGG	CGCGCGGG	ACGCCCTCG	TGTCGTCGG	GGTGGGATCC	CGGGCGCGT	2100
TTTCCTCTGG	GGCGGGGCG	TGCTCTGGGT	TTCTCCCGA	GGCCCGCCCT	CTCGGGCTC	2160
CGGGGCTGCC	TTGGCTCTG	GGTCTCCG	CTCTGGCGT	CTGTGCCCTC	TTCCCGGCC	2220
CCCCGGCCGCC	GATCTCTTC	TTCCCTCCG	GGCTCGTACC	GGCTTCACTG	CGCTTGGTGG	2280
CCCCGGCTGC	GACGACACC	GGCACCGCT	CGTGGGCC	CGCCGCCG	CACTGATCGG	2340
CCCCGGCTGC	CGCTGGCCCG	CGCGGCCGCT	TGGGGACCGG	GTGGTGGGCC	CGGCCGCTGG	2400
GGGGGGTGG	CGCTCCCGGA	GGGTTCCGG	GGTGGCGCTC	GGCGCGCTG	GGGGGAGGAG	2460
ACGGTCTCGG	GGGACAGGGT	TGTCGACG	GGGGGGCGGT	GGTGGGGGGA	GGCGCGGGGA	2520
CGCGCGAGGG	CGCGCTGGCC	CCCCGGGTG	CGCGCGCGT	CGCGCGCG	CGGTGAGGCC	2580
CGCGCGTGT	GTCCCGCTG	CGGTGCGCG	CGTCGAGGG	GTCCCCCTG	CGTCCCCCTTC	2640
CCCCGGGCC	GCTTTCTCG	CGCTCTCCC	GTGCGCCCG	CGTCGCCCCG	GGTCTCTCGT	2700
CTTCTCCGG	CCCCGCTCTC	CGAACCGGT	CGCGCGCTC	CGCGGGTGC	CTCTGCTTCC	2760
GGGGGCTGCC	CGCGGCCCTTC	CGCGAGGGGT	CGTCTCCGGG	CGTGGCGCTG	GGGGAGAGGCC	2820
CGTCTCTCCC	CGCTGGCGTC	CCCCGGTTC	CGCGCGCGT	CGGCCCGAGC	CGGCCCGGGT	2880
GGTCCTCTCC	GGACAGGGCT	TGTCGACG	TGTGGCTGG	GTGACCTCC	GCCTTGGCG	2940
CTGCTCGCCC	TCTCCCGG	TGGGGGGTG	GGGCCCGGG	CGGGGCTCG	GCCCCGGTC	3000
CTGCTCTCCG	TCCCCGGGG	GGGGGGGGG	GGCGCGCCG	CTCGGTGCC	CTCCCTTGGC	3060
CTGCTGTGG	CGTGTGCCA	CCCCGCGCG	GGCGCCGCC	GGGGGGTGC	GAGCGGGGCT	3120
TCGGCGGGC	CCCCGGCCCT	CGACCGGACC	GGCTGCGCG	GGCTGCGGC	CGCACGGCG	3180
GACTGCTCCC	GGGGGGCGGA	CGCGGGTCTC	CTCTGCTG	GGCGCCGGGA	CGTGGGGGCC	3240
CCCCGGCGGG	CGGGCGCGAG	CGCGCTCCC	GGCTCGCG	CGCCGCCG	CGCGGGCGC	3300
CGCGCGCGC	CGCGCGCCG	CGGCTCC	GGGGGGTGC	GGCGGTCCG	GGCCCCGGTG	3360
CTCTCTCGGG	CGGGGGCGGA	CGAAGAACGC	TGCGGGTCT	GTGCGCGGG	GCCCCCGGGT	3420

GTCGTGTCG	GTTGGGGCG	GGTGGTTGG	GGCTCGGTT	C CGCGCGCC	CGCCCGGGC	3480
CCACCGTCC	CGGCCCGCG	CCCCCGCGCC	GCTCGTCCC	TCCCGTCCG	CGTCGGCG	3540
CCCGTCCGTC	CGTCGTCCTC	TGCTGCTCTC	CGCTTGCGG	GGCGCGGGC	CGTCCTCGCG	3600
AGGGCCCG	GGCGCGCG	CGCGCGCG	GGGGGGCG	CGCGCTCTAC	CTTACCTACC	3660
TGGTGTATC	TGCGGCTAG	ATATGCTTGT	CTCAAAGATT	AAGCCATGCA	TGCTTAAGTA	3720
CGCACGGCG	GTACAGTGA	ACTGCGAATG	GTCATTA	TCAGTTATG	TCTCTTGTG	3780
CGCTCGTCC	TCTCTTACT	GTTAACTGT	GTTAACTTCA	GAGCTAAATAC	ATGCGGACCG	3840
GCCTGACCC	CCCTCGGGG	GGGGATCGT	GCATTTATCA	GATCAAACAC	AACCGCGTA	3900
GCCCCCTCT	GGCCCCGGC	GGGGGGGGG	CGCCGGCGG	TTTGGTGACT	CTAGATAACC	3960
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CTTTCATGG	TAGTCGCGT	GCCTACCATG	GTGACCAACGG	GTGACGGGA	ATCAGGGTTC	4080
GATTCGGGAG	AGGGAGCGT	AAAGAACGCT	ACCACATCCA	AAGAACGGAG	CAGGGCGCGA	4140
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TTCTTGACCC	GGGGCAAGAC	GGACAGAGC	GGAAAGATT	GCCAAAGAATG	TITTCATTA	4680
TCAAGAACGA	AAGTCGGAGG	TTGCAAGAC	ACTAGATACC	GTCTGAGTT	CGACCATAAA	4740
CGATGCCGAC	CGGGCGATGC	GGCGCGTTAT	TCCCCATGAC	CGCCGGGCG	CTTCCCGGAA	4800
CAAAAGTCT	TGTTGGTTCG	GGGGGGATAT	GGTTGCAAG	TGAAACTTA	AAGGAATTG	4860
CGGAAGGGCA	CCACCAAGAG	TGGAGCGCTC	GCGCTTAATTT	GACTCAACAG	GGGAAACCTC	4920
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GTGTTGATG	CGCTTCTTA	TTGGTGTGAG	CGATTGTTCT	GGTTAATTCC	GATAACGAA	5040
GAGACTACG	CATGCTTCA	AGTTACCGGA	GGGGGGCG	GTGCGGTC	CCCAACTTCT	5100
TAGAGGACACA	AGTGGCGTC	AGGACCCCGA	GATTTGACAA	TAACAGGCT	GTGATGCC	5160
TAGATGTC	GGGGCTGCA	CGCGCTAC	TGACTGCGTC	ACGGCTGTG	TACCCCTACG	5220
CGGCGGGCG	GGGTTAACCG	TGAAACCCC	TTCTGTATG	GJATCGGGG	TTGCAATTAT	5280
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CTCTGGCTT	GTACACACCG	CCCGTCTGCA	CTACCGATTG	GATGTTTTAG	TGAGGCCCTC	5400
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GCCGCGGG	CTCCCCGTCT	TCGGGGCGG	CGGGAATCCC	GTGCGCTTCCG	CCCGCGCGT	6000
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CGTGGGTCG	GGGGCGGTG	GGGGCCCGC	GGGGAGTCCC	TCGGAGGGG	CCGGCCCCCT	6240
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CGCGGGCGG	CGGGGGGG	GGGAACCCCC	GGGGCGCTGT	GGGGTGTTGT	CCCGCGCTCG	6420
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CGCAAGGCC	CGGGGGGGG	CTCCGTCCC	CTAAGCGAG	ACCCGGGGC	GTCCGGCCCT	6900
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TAAGCGCGGC	CGCGCCCGCT	CCGGCGCTCG	CTGGCGCGC	GTGGCGCGG	CGCGGGAGCC	7500
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CACTGTGTC	GTTCTTGTGTC	TTACTCTCTT	TCTCTTGCCT	GGCCTCTGT	CTGTCCTGTC	26880
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TTGTTGTTGT	TGGGGACTTT	CTCTGATTC	CCAGGAGTGA	GTGAAAGCAG	GTAGATTTGCC	39480
TTGCGCTGGC	TTGCGCTGGC	TTGCTCTTTC	TTCTCTTCTT	TTCTTCTTAA	TTACTTTCTC	39540
TTTTCTCTCT	TCCTCTCTT	CTTTTTTTTG	AGACAGAGTT	TCACCTCTGT	TGCCCCAGGT	39600
AGAGGGCAAT	GGCGCAGATC	CGCGTCACCG	CACCCCTCGC	CTCCAGGTT	CAAGCGATTIC	39660
TCTCGCTCTA	GCCTCTCTGAT	TACGTGGGAT	TCAGGCGATC	GGGCCAGGTG	CTGCGTATG	39720
TTTGTACTCT	TAGTAGAGAC	GGTTTTTTTC	CAATGTTGTC	AGGCTGGTCT	CCCCACTCCCA	39780
ACCTCAGTGT	CGTCGGCTGC	CTTAGCTCC	CAAAAGTCTC	GGATGACAGG	CGTGAACCCG	39840
CGCCGACGCC	CTCTCTCTCT	CTCTCTCTCT	CTCGCGCTGC	TGCTGCTT	CTTTCGCTGT	39900
TTCTGCTTCT	CCCTCTTCTCT	TGCTTCTTCTT	CTTCTCTTCG	TTCTCTTCTAT	GTTGCTTCTTC	39960
TTGCTTGTCT	GTCTGCTTCT	GTCTCTTCTT	GTCTTCTCTG	TTCTCTTCTT	TTCTCTTCTC	40020
TTCTCTCTCT	TTGTTTCTT	CTCTGCTGCT	TTCTGTGTTG	CTCTGCTGCT	TTGCTGCTTT	40080
CTTGTCTTCC	TGTTTCTTCTT	CTTCTCTTCTT	TTCTTCTCTT	TCTTCTTCTG	TGCTCTTCTT	40140
GCTTGTCTGC	TTTGTGCTT	TCTGTGTTTC	TGTTTCTCTT	TCTTCTTCTT	TGTTTCTTCTC	40200
TGTTGCTTCTT	CTCTGCTGCT	TGCTTCTGTTG	CTTCTCTGCT	TCTGTGTTTC	TTTCTTCTCTT	40260
TCTCTCTTCTT	TGTTTCTCTT	TCCTGCTGTT	CTCTGCTGCT	TGCTTCTGTT	CTGCTCTGTT	40320
TCTCGATTT	TTCTCTCTCT	TTGTTTCTT	CTCTGCTGCT	TCTCTCTCT	ATTGCTTCTG	40380
TGCTTCTCTT	CTTCTCTCTT	TTCTTCTTCTT	CTTCTGTTTC	TTCTCTTCTT	GCTTCTCTGT	40440
TTTCTCTCTT	TTCTGCTGTC	GTCTTCTCTG	GTCTTCTCTG	TTCTCTGCTT	TTCTCTTCTT	40500
GTTTCTCTCT	TGCTGCTTCT	CTTCTGCTCT	TGTTTCTCTG	TCTTCTGCTT	TGCTTCTCTT	40560
CGTCTCTCTT	TTCTGCTTCT	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	40620
CTTTCTCTTC	ATCATCATCT	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	40680
TTCTTCTCTT	TCTTCTCTTC	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	40740
TTCACTCTTG	TCTTCTCTGC	TAAGAGTCAA	TGAGCTGCAA	TGCGCGATC	GCACCTTCCG	40800
CCTCTGGGT	TGAGCGCTCT	CTCTCTCTCT	CAAGCTCTCC	ATTAGGGGGG	ATTGACAGGG	40860
AGGGACCCCC	AGGCGCTGCT	TGCTGTATG	TGTTGTTTT	AGTAGGCAC	CGGTGCTCT	40920
CCATGTTGCT	CAGGGCTGGTC	TCCAACTCTCC	GACCTCTGTG	GATGCGCCCA	CTTCGGCCCTC	40980
TCGAAGTGT	GGGATGACGG	GGCTGAGCAC	CGTGGCCGGC	CTGTTGACTC	ATTTCGCTT	41040
TTTATCTCTT	TCGTTTCTAC	GGCTGTTACTT	ATATGTATTA	ATGTAACAGT	TTCTGTACCG	41100
TTATATGCAA	AAACAGCACA	CGTGTATCTC	TGCTGATTA	ACTCTTGCGT	ATGGTAAATA	41160
CGTATCGGTT	GTATGGAAT	AGACTCTCTG	ATGATAGATG	TGTTGCTCTG	TGTTATACAA	41220
ATAAATACAC	TTAGGAGTAT	AGAGAAGGGG	TGCTGATATA	AGACGTTTAT	TTAACGTAATG	41280
AAAAGCTCG	TATTTATGIG	TGTTAATGAA	CGGAGCTGAC	TDAGTTATCT	CTGTTTCTT	41340
TCTCTCTCTC	CTTCGCTGTT	TTCTTCTCTTC	TTCTTCTCTT	TTCTTCTCTT	TTTAACTGTT	41400
TTCTCTCTCT	TCCTCTCTCT	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	TTGCTTCTT	41460
TTCTCTCTTC	TTCTCTCTCT	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	TTGCTTCTT	41520
TTCTCTCTCT	TTCTCTCTCT	TTCTTCTCTT	TTCTTCTCTT	TTCTTCTCTT	TTTCCCCT	41580
GTCTTCTTAA	AAATTGAGAT	GTTTCAAGAAG	TTTACTCTTG	GTATCTACGT	TTCTAAATT	41640
GTCTCTCTT	TCCTCCATT	CTTCTCTCTC	CCCTCTCTCC	CTCTCTGCTC	CTCTCTCTCC	41700
CTCTCTCTCT	TCGGCATCT	GTCTCTCTTC	CCCACTCTCC	TCCCCCTGTC	TGTCCTCTGG	41760
TGGATTCGG	AAAGAGCTTAC	CGATTCTGCG	TCTCCGTGTG	TCTGAGCGA	CCCCGGGAC	41820
GAGTCCCTGT	GTGTTCTTTC	TCCCTCTCTC	CTTCCCTCTCC	TCCCTCTCTC	CTTCCCTCTG	41880
TCCGAGAGGC	ATCTCCAGAG	ACCGCGCCGT	GGGTTGTTCTT	CTGACTCTGT	CGCGGTCGAG	41940
GCAGAGACGC	GGTTTGGGGCA	CGCTTGTGTT	GGGGTGGGGG	CAAGAGGGCT	GGTTTTCTGG	42000
CCTCGGGAAAG	AGCTTCTCGA	CTCACCGTTT	CGCTTCTCGG	GTCCAGGGGC	CGCCCTGCGCA	42060
GGCCGAGATCG	TCTCGCTGAC	GTCCGGCGCG	GTGTCGCGGC	TCCATCTGGC	GGCCGCTTITG	42120
AGATCTGTC	CTGGCGCTTC	GGAGCTGCGG	TGGCAGCTGC	CGAGGGAGGG	GACCGTCCCC	42180
GCTGTGAGCT	AGGCAGAGCT	CGGAGAAGGC	CGGGCGTCG	AGCCCGGGCTG	GGCCGGTGGC	42240
GCCAGAGCTG	TGGCGCTGCG	CTGTGCTG	ACAGCTCTGG	CTGCGAGGT	TATGTTGGGG	42300
AGAGGCTGTC	GCTGCGCTTC	TGGGGCCGGG	GGGGCGTGTG	GGCTGCCCGG	GCCGTCGAC	42360
CAGCGGCCG	TAGCTCCCGA	GGCCCGAGCC	GGACCCGGC	GGACCCGGCG	CGCGTGGCGG	42420

AGGCTGGGGA	CGCCCTTCCC	GGCCCGGTGCG	CGGTCGCCCTC	ATCCCTGGCCG	TCTGAGGCGG	42480
CGGCCAATT	CGTTTCCGAG	ATCCCCGTGG	GGAGCCGGGG	ACCGTCCCGC	CCCCGTCCCC	42540
CGGGCGCC	GGAGCGCCCG	CCGGCGGTCCC	CCGGCGGTCCC	TCTGCGGCCGA	TCTTTTCTGG	42600
CGAGTCCCCG	TGGCCAGTCG	GAGAGCGCTC	CCTGAGCGGG	TGCGGCCCGA	GAGGTGCGGC	42660
TGGCGGCCCT	TGGCTCCCTC	GTGTGTCGCCG	GTCTGAGGAG	GGGCCCGGGCG	AAAATGCTTC	42720
CGGCTCCCG	TCTGGAGACA	GGGGCGGCCG	CCTGCGTGTG	GCCAGGGCGG	CCGGAGGGCG	42780
TCCCGGGCCC	GGCGCTGTCC	CCCGCGTGTG	CCTTGGGTTG	ACAGAGGGGA	CCCGGGCGCG	42840
TCCGTGTGTTG	GCTGGATGG	TGGCGTTTT	GGGACAGGT	GTCCGTGTCC	GTGTCGCGCG	42900
TCGCCTGGGC	CGGCGGCCTG	GTCCGTGACG	CGACCTCCCG	GCCCGGGGGG	AGGTATATCT	42960
TTCGCTCCGA	GTCCGCAATT	TTGGGCGCC	GGGTTATAT			42999

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCGCGCG	GCCCCCGTGT	TCGCCGTTC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGT	TCCCGTGCAGT	GGCCGTTGTTG	AGTGGCTTCGC	TCTCCCTCCTC	CTCCCCGGCA	120
CGCTTCCAC	GGTGGGGAC	CACGGTGAC	CTGCCCTCT	TCGGGCTTG	ATCCG	175

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGAAAC	GGCGGGGTG	60
GTCGCGCCCG	GGCGCGGAGC	TGTGTCGGCG	CCCACTCTCC	GCTCGAGGGT	GGCGGTGGGG	120
GGCGCGTGGG	TAGTCTCCCG	TGTTGCGCTC	TCTGGGCGTC	TTGGGGGGGG	TGCCGTGCGT	180
TTCGGGCCCG	GGCTGTGCTT	GCTTACCGAG	GCTTGGTTG	GAACTGCGCTC	AGGAGTCGTG	240
GGCGGTGTGA	TTCCCGCCGG	TTTGCGCTCG	CCTGCTGCCCG	CTTGGCCTG	GGTTTGCCTG	300
GTTCTGTCT	CGGGAGGGT	GGTTTTTTT	TTTTGCGGT	CCCGGGGAGA	GGGGTTTTTC	360
CGGGGGACGT	TCCCGTGCGCC	CCCTGCGGCCG	GGTGGGTTTT	CTTTTCGGGC	TGTGTTGCGT	420
TCCCCCTTCCC	CGTTTCCCGC	TCGGTCTCTC	CCGGTGGCTC	GCCCCCTCTCC	CCGGTGGTC	480
GCCCCGGCGT	GCTGCGGGAC	CCCCCCTTCT	GGGGGGGATG	CCCGGGCAGC	CACGCGTCGG	540
GGCGGGCACT	GTGTCGCGG	AGCTGCTCGG	CAGGGCGGTG	ACCGAGTTG	AGGGCGCTGA	600
TGCCCCCGCG	GGCTCCCGTG	GCCGACCGCG	CGTGTCTCTT	GGGGGGGCCT	GTGCGTGCAG	660
GAAGGCTGCG	CACGTTGTCG	GTCTTGTGCGA	GGGAAAGAGG	CTTTTTTTT	TTAGGGGTC	720
GTCTCTCGTC	GTCCCGTCGG	CGGTGGATCC	GGCCT			755

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCGGAGGTG	CGTCTGCCGG	TTGGGGCTCC	TCCGGCCCCC	TCTGCCCTCCG	GGAAAGGCCGT	60
TAGCGGGTAC	CGTGCCCGC	CGGAGGTGGG	CGCACGTGG	TGAGATAACC	CCGAGCTGT	120
TTCTCGTTGT	TGGCGCCGGG	GGCTCCCGTC	GAATGCTTCC	CTCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAAGCC	TCCGCCCTG	GGCTTCGTGG	GGCGTCTCCC	CCCCCTCTAC	GTCCTCTCGC	240
AGCGAGCCCG	TCCGTTGAC	CTTCCCTTCCG	CCTTCCCCCC	ATCTTTCCGC	GCTCCGTTGG	300
CCCGGGGGTT	TTCACGGCC	CCCCAACGCT	CTCCGCGCTC	TCCGGCCGTG	GTTTGACGCG	360
CTGGTTCCGG	TCTCCCCC	AAACCCCGGT	TGGGGTTGGT	TCCGGCCCCG	GCTTGTCTT	420
CGGGTCTCCC	AACCCCGGC	CGGAAAGGGT	CGGGGGTTCC	GGG		463

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCT	TCCGGCTTCC	GGCCGGGGGG	60
GGCGGGCCCG	GGCGGTTGG	TGAGTTAGAT	AACTCTGGC	CGATCGACG	CCCCCGTGG	120
CGGGGACGAC	CCATTAACGAC	GTCTGCCCTA	TCAACTTTCG	ATGGTAGTCG	ATGTGCTTAC	180
CATGGTACCC	ACGGGTGACG	GGGAATCAGG	GTTCGATTCC	GGAGAGGGAG	CCTGAGAAAC	240
GGCTTACACA	TCCAAGGAG	GCAGCAGCG	CGCAAATTAC	CCACTCCGA	CCGGGGAGG	300
TAGTGACGAA	AAATAAACAT	ACAGGACTCT	TTCGAGGCC	TGTAATTGGA	ATGAGTCCAC	360
TTAAATCT	TTAAGCAG					378

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCCAGC	AGCCGCGGTA	ATTCCAGCTC	CAATAGCGTA	60
TATTAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGGGAGCGGG	CGGGCGGTCC	120
GCCGCGAGGC	GAGTCACCGC	CCGTCCTCCC	CCCTTGCCTC	TCCGGCCCCC	CTCGATGCTC	180

TTAGCTGAGT	TGTCCCGCGG	GGCCCGAAGC	GTTTACTTTG	AAAAAAATTAG	AGTTGTTTCA	240
AAGCAGGCC	GAGCCGCCTG	GATACCGCCA	GCTAGGAAAT	AATGGAATAG	GACCGCGGTT	300
CCTTATTGTC	TTGGTTTTCG	GAACTGAGCC	CATGATTAAG	GGAACCGGCC	GGGGGCATTG	360
CCTTATTGCG	CCCCCTCA					378

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTCTC	CGCTCCCCGT	TCCCTCCCGG	CCCTCCACCC	GCGCGTCTCC	CCCCCTTCTT	60
TCCCTCTCTC	CGGAGGGGGG	GAGGTGGGGG	CGCGTGGGGC	GGGTCGGGGG	TGGGGTCTGGC	120
GGGGGACCGC	CCCCGGCGG	CAAAAGCCG	CCGCCGGCG	CACTTCACCC	GTAGCGGTGC	180
GCCGGACGCC	GCTACAGAGC	GCGTGGGAAG	GCCCCGACGGG	GAATGTGGCT	CGGGGGGGGC	240
GGCGCGTCTC	AGGGCGGCC	GAACCCACTC	ACCCCGAGTG	TTACAGCCCT	CCGCCGC	300
TTTCGCGAA	TCCCGGGGCC	GAGGGGAAGC	CCGATAACCG	TCGCCGCCT	TTTCCCCTCC	360
CCCCGTCTC	CCCCGGGGC	GGCGTGGGG	TGGGGGCCGG	GGGGCCCCCTC	CCACGCCCCG	420
GGTTTCTCTC	TCTCCCGTCTC	TGCCCGGT	TGGGGGGGGG	AGCCCCGTTG	GGGGCGGGGC	480
GGATCTGCTT	CAGTGCGCC	CGGGCGTCTG	CGGCCCGTCC	GGCCCGGGGGG	GTTCCTCTCGG	540
TCACCGCCCG	CCCCGACAC	CCGAGCGCAC	GGGGTCGCGC	GGCATGTCGG	CTACCCACCC	600
GACCGCTCTT	GAACACACCGA	CCAAGGAGTC	TAACCGCTGC	GGCAGTCAGG	GGCTCCACG	660
AAAGCCGCCG	TGGCGCAATG	AAAGTGAAGG	GGCCCGTCCG	GGGGCCCGAG	GTGGGATCC	719

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCCTCT	CCAGTCCGCC	GAGGGCGCAC	CACCGGCCG	TCTCGCCCGC	CGCGTCGGG	60
AGGTGAGCCA	CGAGCGTACG	CGTFAAGGAC	CGAAAGATGG	TGAACATATGC	CTGGGCAGGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCC	GTAGCGGTCC	TGACGTGCAA	ATCGGTGCTC	180
CGACCTGGGT	ATAGGGCGA	AAAGACTAATC	GAACCATCTA	GTAGCTGGTT	CCCTCCGAAG	240
TTTCCCTCAG	GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CACTTTTATC	CGGGTAAAGG	300
CGGAATGGAT	TAGGAGGTCT	TGGGGCGGGA	AAAGATCTCA	AACTATTTCT	CAAACCTTAA	360
ATGGGTAAGG	AAAGCCCGCT	CGCTGGCGT	GAAGCCGGGC	TGGAAATGCGA	GTGCCCTAGTG	420
GGGCCATTTT	GGTAAGCAGA	ATGCGCTG	CGGGATGAAAC	CGAACCCGGG	GTAAAGCGC	480
CCGATGCCGA	CGCTCATCAG	ACCCCGAAAGA	AGGTGTGGT	TGATATAGAC	AGCAGGACGG	540
TGGCCATGGA	AGTCGGRAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAAA	TGGATGGCGC	TGGAGCGTCG	GGGCCATACC	CGGGCAGTCGC	CGGCAGTCGG	660
AACGGGACGG	GACGGGAGCG	GCGC				685

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

- (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG

35

- (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCA AGAAGAGAGG TGGCTCGGCC TGC

33

- (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAAACC CTAACCCCTAA CCCTAACCCCT AACCCCTAAC CTAACCCCTAA
CCCTAACCCCT AACCCGGGAT60
80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21